

Figure 1(A)

<u>GGATCGTCTCAGGTCAGCGGAGGGA</u>	25
SL33	
<u>GGAGACTTATAGACCTATCCAGTCT</u>	50
TCAAGGTGCTCCAGAAAGCAGGAGT	75
TGAAGACCTGGGTGTGAGGGACACA	100
TACATCCTAAAAGCACCACAGCAGA	125
GGAGGCCCCAGGCAGTGCCAGGAGTC	150
AAGGTTCCCAGAAGACAAACCCCT	175
AGGAAGACAGGCGACCTGTGAGGCC	200
<u>CTAGAGCACCACTTAAGAGAAGAA</u>	225
SL34	
GAGCTGTAAGCCGGCCTTTGTCAGA	250
GCCATCATGGGGGACAAGGATATGC	275
CTACTGCTGGGATGCCGAGTCTTCT	300
CCAGAGTTCCTCTGAGAGTCCTCAG	325
AGTTGTCCTGAGGGGGAGGACTCCC	350
AGTCTCCTCTCCAGATTCCCCAGAG	375
TTCTCCTGAGAGCGACGACACCCTG	400
TATCCTCTCCAGAGTCCTCAGAGTC	425
GTTCTGAGGGGGAGGACTCCTCGGA	450
TCCTCTCCAGAGACCTCCTGAGGGG	475
AAGGACTCCCAGTCTCCTCTCCAGA	500
TTCCCCAGAGTTCTCCTGAGGGCGA	525
CGACACCCAGTCTCCTCTCCAGAAT	550
TCTCAGAGTTCTCCTGAGGGGAAGG	575
ACTCCCTGTCTCCTCTAGAGATTTT	600
TCAGAGCCCTCCTGAGGGTGAGGAT	625
GTCCAGTCTCCTCTGCAGAATCCTG	650
CGAGTTCCTTCTTCTCCTCTGCTTT	675
ATTGAGTATTTTCCAGAGTTCCCCT	700

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Figure 1(B)

GAGAGAACTCAGAGTACTTTTGAGG 725
GTTTTCCCCAGTCTCCTCTCCAGAT 750
TCCTGTGAGCTCCTCCTCCTCCTCC 775
ACTTTATTGAGTCTTTTCCAGAGTT 800
CCCCTGAGAGAACTCAGAGTACTTT 825
TGAGGGTTTTCCCCAGTCTCTTCTC 850
CAGATTCCTATGACCTCCTCCTTCT 875
CCTCTACTTTATTGAGTATTTTCCA 900
GAGTTCTCCTGAGAGTGCTCAAAGT 925
ACTTTTGAGGGTTTTCCCCAGTCTC 950
CTCTCCAGATTCCTGGGAGCCCCCTC 975
CTTCTCCTCCACTTTACTGAGTCTT 1000
TTCCAGAGTTCCCCTGAGAGAACTC 1025
ACAGTACTTTTGAGGGTTTTCCCCA 1050
GTCTCCTCTCCAGATTCCTATGACC 1075
TCCTCCTTCTCCTCTACTTTATTGA 1100
GTATTTTCCAGAGTTCTCCTGAGAG 1125
TGCTCAAAGTACTTTTGAGGGTTTT 1150
CCCCAGTCTCCTCTCCAGATTCCTG 1175
GGAGCCCCTCCTTCTCCTCCACTTT 1200
ACTGAGTCTTTTCCAGAGTCCCCT 1225
GAGAGAACTCACAGTACTTTTGAGG 1250
GTTTTCCCCAGTCTCCTCTCCAGAT 1275
TCCTATGACCTCCTCCTTCTCCTCT 1300
ACTTTATTGAGTATTTTACAGAGTT 1325
CTCCTGAGAGTGCTCAAAGTGCTTT 1350
TGAGGGTTTTCCCCAGTCTCCTCTC 1375
CAGATTCCTGTGAGCTCCTCTTTCT 1400

Figure 1(C)

CCTACACTTTATTGAGTCTTTTCCA 1425
GAGTTCCCCTGAGAGAACTCAGAGT 1450
ACTTTTGAGGGTTTTCCCCAGTCTC 1475
CTCTCCAGATTCCTGTGAGCTCCTC 1500
CTCCTCCTCCTCCACTTTATTGAGT 1525
CTTTTCCAGAGTTCCCCTGAGTGTA 1550
CTCAAAGTACTTTTGAGGGTTTTCC 1575
CCAGTCTCCTCTCCAGATTCCTCAG 1600
AGTCCTCCTGAAGGGGAGAATACCC 1625
ATTCTCCTCTCCAGATTGTTCCAAG 1650
TCTTCCTGAGTGGGAGGACTCCCTG 1675
TCTCCTCACTACTTTCCTCAGAGCC 1700
CTCCTCAGGGGGAGGACTCCCTATC 1725
TCCTCACTACTTTCCTCAGAGCCCT 1750
CCTCAGGGGGAGGACTCCCTGTCTC 1775
CTCACTACTTTCCTCAGAGCCCTCA 1800
GGGGGAGGACTCCCTGTCTCCTCAC 1825
TACTTTCCTCAGAGCCCTCCTCAGG 1850
GGGAGGACTCCATGTCTCCTCTCTA 1875
CTTTCCTCAGAGTCCTCTTCAGGGG 1900
GAGGAATTCCAGTCTTCTCTCCAGA 1925
GCCCTGTGAGCATCTGCTCCTCCTC 1950
CACTCCATCCAGTCTTCCCCAGAGT 1975
TTCCCTGAGAGTTCTCAGAGTCCTC 2000
CTGAGGGGCCTGTCCAGTCTCCTCT 2025
CCATAGTCCTCAGAGCCCTCCTGAG 2050
GGGATGCACTCCCAATCTCCTCTCC 2075
AGAGTCCTGAGAGTGCTCCTGAGGG 2100

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Figure 1(D)

GGAGGATTCCTGTCTCCTCTCCAA 2125
 ATTCCTCAGAGTCCTCTTGAGGGAG 2150
 AGGACTCCCTGTCTTCTCTCCATTT 2175
 TCCTCAGAGTCCTCCTGAGTGGGAG 2200
 GACTCCCTCTCTCCTCTCCACTTTC 2225
 CTCAGTTTCCTCCTCAGGGGGAGGA 2250
 CTTCCAGTCTTCTCTCCAGAGTCCT 2275
 GTGAGTATCTGCTCCTCCTCCACTT 2300
 CTTTGAGTCTTCCCCAGAGTTTCCC 2325
 TGAGAGTCCTCAGAGTCCTCCTGAG 2350
 GGGCCTGCTCAGTCTCCTCTCCAGA 2375
 GACCTGTCAGCTCCTTCTTCTCCTA 2400
 CACTTTAGCGAGTCTTCTCCAAAGT 2425
 TCCCATGAGAGTCCTCAGAGTCCTC 2450
 CTGAGGGGCCTGCCCAGTCTCCTCT 2475
 CCAGAGTCCTGTGAGCTCCTTCCCC 2500
 TCCTCCACTTCATCGAGTCTTTCCC 2525
 AGAGTTCTCCTGTGAGCTCCTTCCC 2550
 CTCCTCCACTTCATCGAGTCTTTCC 2575
 AAGAGTTCCCCTGAGAGTCCTCTCC 2600
 AGAGTCCTGTGATCTCCTTCTCCTC 2625
 CTCCACTTCATTGAGCCCATTAGT 2650
 GAAGAGTCCAGCAGCCCAGTAGATG 2675

SL26

AATATACAAGTTCCTCAGACACCTT 2700
 GCTAGAGAGTGATTCCCTTGACAGAC 2725
 AGCGAGTCCTTGATAGAGAGCGAGC 2750
 CCTTGTTCACTTATACTGGATGA 2775
 AAAGGTGGACGAGTTGGCGCGGTTT 2800

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Figure 1(E)

CTTCTCCTCAAATATCAAGTGAAGC	2825
SL27	
AGCCTATCACAAAGGCAGAGATGCT	2850
GACGAATGTCATCAGCAGGTACACG	2875
GGCTACTTTCCTGTGATCTTCAGGA	2900
AAGCCCGTGAGTTCATAGAGATACT	2925
TTTTGGCATTTCCTTGAGAGAAGTG	2950
GACCCTGATGACTCCTATGTCTTTG	2975
TAAACACATTAGACCTCACCTCTGA	3000
GGGGTGTCTGAGTGATGAGCAGGGC	3025
ATGTCCCAGAACCGCCTCCTGATTC	3050
TTATTCTGAGTATCATCTTCATAAA	3075
GGGCACCTATGCCTCTGAGGAGGTC	3100
ATCTGGGATGTGCTGAGTGGAATAG	3125
GGGTGCGTGCTGGGAGGGAGCACTT	3150
TGCCTTTGGGGAGCCCAGGGAGCTC	3175
CTCACTAAAGTTTGGGTGCAGGAAC	3200
ATTACCTAGAGTACCGGGAGGTGCC	3225
CAACTCTTCTCCTCCTCGTTACGAA	3250
TTCTGTGGGGTCCAAGAGCTCATT	3275
CAGAAGTCATTAAGAGGAAAGTAGT	3300
AGAGTTTTTGGCCATGCTAAAGAAT	3325
ACCGTCCCTATTACCTTTCCATCCT	3350
CTTACAAGGATGCTTTGAAAGATGT	3375
GGAAGAGAGAGCCCAGGCCATAATT	3400
GACACCACAGATGATTCGACTGCCA	3425
CAGAAAGTGCAAGCTCCAGTGTCAT	3450
GTCCCCCAGCTTCTCTTCTGAGTGA	3475
AGTCTAGGGCAGATTCTTCCCTCTG	3500

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Figure 1(F)

AGTTTGAAGGGGGCAGTCGAGTTTC 3525
TACGTGGTGGAGGGCCTGGTTGAGG 3550
CTGGAGAGAACACAGTGCTATTTGC 3575
ATTTCTGTTCCATATGGGTAGTTAT 3600
GGGGTTTACCTGTTTTACTTTTGGG 3625
TATTTTTCAAATGCTTTTCCTATTA 3650
ATAACAGGTTTAAATAGCTTCAGAA 3675
TCCTAGTTTATGCACATGAGTCGCA 3700
CATGTATTGCTGTTTTTCTGGTTTA 3725
AGAGTAACAGTTTGATATTTTGTA 3750
AAACAAAACACACCCAAACACACC 3775
ACATTGGGAAAACCTTCTGCCTCAT 3800
TTTGTGATGTGTCACAGGTTAATGT 3825
GGTGTTACTGTAGGAATTTTCTTGA 3850
AACTGTGAAGGAAGTCTGCAGTTAA 3875
ATAGTGGAATAAAGTAAAGGATTGT 3900
TAATGTTTGCATTTCCCTCAGGTCCT 3925
TTAGTCTGTTGTTCTTGAAAATAA 3950
AGATACATACCTGGTTTGCTTGGCT 3975
TACGTAAGAAAGTAGAAGAAAGTAA 4000
ACTGTAATAAATAAAAAAAAAAAAAA 4025
AAAAAA 4031

FIG. 2(A)

[illegible]

1

A1
C1 AGTCTTTCCAGAGTTCCCC TGAGAGAAGTCCAGAGTCTT TTGAGGGTTTTCCTCCAGTCT CCACTCCAGATTCCTGTGAG CCGCTCCTTCTCCTCCACTT 1094
S L F Q S S P E R T Q S T F E G F P Q S P L Q I P V S R S F S S T L 280

A1
C1 TATTGAGTATTTCCAGAGT TCCCTGAGAGAAGTCCAGAG TACTTTGAGGGTTTTCCTCCAGATTCCT GTGAGCTCCTCCTCCTCCTC 1194
L S I F O S S P E R T Q S T F E G F A Q S P L Q I P V S S S S S S 313

A1
C1 CACTTATTGAGTCTTTCC AGAGTCCCTGAGAGAAGT CAGAGTACTTTTGAGGGTTT TCCCAGTCTCTCCTCCAG TTTCTATGACCCTCCTCCTC 1294
T L L S L F Q S S P E R T Q S T F E G F P Q S L L Q I P M T S S F 346

A1
C1 TCTCTACTTTATTGAGTAT TTCCAGAGTCTCCTGAGA GTGCTCAAAGTACTTTTGAG GGTTCCTCCAGTCTCCTCT CCAGATTCTGGGAGCCCCCT 1394
S S T L L S I F Q S S P E S A Q S T F E G F P Q S P L Q I P G S P S 380

A1
C1 CCTCTCCTCCACTTACTG AGTCTTTCCAGAGTTCCCC TGAGAGAAGTCCAGAGTCTT TTGAGGGTTTTCCTCCAGTCT CCTCTCCAGATTCCTATGAC 1494
F S S T L L S L F Q S S P E R T H S T F E G F P Q S P L Q I P M T 413

A1
C1 CTCCTCCTTCTCCTCCTACTT TATTGAGTATTTTACAGAGT TCTCCTGAGAGTGCTCAAAG TGCTTTTGAGGGTTTTCCTCC AGTCTCCTCCTCCAGATTCCT 1594
S S F S T L L S L L Q S S P E S A Q S A F E G F P Q S P L Q I P 446

A1
C1 GTGAGCTCCTCTCTCCTTA CACTTATTGAGTCTTTCC AGAGTCCCTGAGAGAAGT CAGAGTACTTTTGAGGGTTT TCCCAGTCTCCTCCTCCAGA 1694
V S S S F S Y T L L S L L F Q S S P E R T Q S T F E G F P Q S P L Q I 480

A1
C1 TCTCTGAGGCTCCTCCTCC TCCCTCCAGTCTTTTATGAG TCTTTCCAGAGTCTCCTCCAG AGTGTACCAAGTACTTTT GAGGGTTTTCCTCCAGTCTCC 1794
P V S S S S S T L L S L L F Q S S P E C T Q S T F E G F P Q S P 513

A1
 C1 TCCTCAGATTCCTCAGAGTC CTCCTGAAGGGGAGAGATACC CATTCTCCTCCTCAGATTGT TCCAAGTCTCCTGAGTGGG AGGACTCCCTGCTCCTCAC 1894
 L Q I P Q S P P E G E N T H S P L Q I V P S L P E W E D S L S P H 546

A1
 C1 TACTTCTCAGAGCCCTCC TCAGGGGAGGACTCCCTAT CTCTCCTCCTCCTCCTCAG AGCCCTCCTCAGGGGAGGA CTCCTGTCTCCTCCTACT 1994
 Y F P Q S P P Q G E D S L S P H Y F P Q S P Q G E D S L S P H Y F 580

A1
 C1 TTCTCAGAGCCCTCAGGG GAGACTCCCTGCTCCTCA CTACTTCTCAGAGCCCTC CTCAGGGGAGGACTCCAIG TCTCCTCTCTACTTTCTCA 2094
 P Q S P Q G E D S L S P H Y F P Q S P P Q G E D S M S P L Y F P Q 613

A1
 C1 GAGTCTCTCAGGGGAGG AATCCAGTCTCTCTCCAG AGCCTGTGAGCATCTGCTC CTCTCCACATCCAGTCTC TCCCCAGAGTTTCCCTGAG 2194
 S P L Q G E F Q S S L Q S P V S I C S S T P S L P Q S F P E 646

A1
 C1 AGTCTCAGAGTCTCTCCTGA GGGCCTGTCCAGTCTCTC TCCATAGTCTCAGAGCCCT CCTGAGGGGATGCATCCCA ATCTCCTCCTCAGAGTCTG 2294
 S S Q S P P E G P V Q S P L H S P Q S P P E G M H S Q S P L Q S P E 680

A1
 C1 AGAGTCTCTCAGGGGAG GATCCCTGTCTCTCTCCA AATCTCAGAGTCTCTTG AGGGAGAGGACTCCCTGCT TCTCTCCTCCTCAGAG 2394
 S A P E G E D S L S P L Q I P Q S P L E G E D S L S S L H F P Q S 713

A1
 C1 TCCTCCTGAGTGGGAGGACT CCCCTCTCCTCTCCACTTT CCTCAGTTCTCCTCCTCAGG GGAGGACTTCCAGTCTCTC TCCAGAGTCTCTGAGTATC 2494
 P P E W E D S L S P L H F P Q F P P Q G E D F Q S S L Q S P V S I 746

A1
 C1 TGCTCTCTCTCCACTTCTT GAGTCTCTCCAGAGTTTCC CTGAGAGTCTCAGAGTCTCT CCTGAGGGGCTGCTCAGTC TCTCTCCAGAGACCTGTCA 2594
 C S S T S L S L P Q S F P E S P Q S P P E G P A Q S P L Q R P V S 780

A1
 C1 GCTCTCTCTCTCTACACT TTAGGAGTCTCTCTCCAAG TTCCATGAGAGTCTCTCAGA GTCTCTCCTGAGGGGCTGCC CAGTCTCTCTCTCCAGAGTCC 2694
 S F F S Y T L A S L L Q S S H E S P Q S P P E G P A Q S P L Q S P 813

A1

C1 TGAGAGCTCCCTTCCCTCCCT CCTTTCATCGAGTCTTTCC CAGAGTTCTCTCTGTGAGCTC CTTCCTCCCTCCTCCACTTCAT CGAGTCTTTTCCAGAGTTCC 2794
[V _ _ _ S _ F _ P _ S _ S _ T _ S _ S _ S _ L _ S _ Q _ S _ S _ P _] V _ S _ S _ F _ P _ S _ S _ T _ S _ S _ S _ I _ S _ K _ S _ S _ 846

A

AT
CCTGAGAGTCCCTCCAGAG TCCTGTGATCTCCTTCCT AGTGAGGGTTCCAGCAG CCGTGAAGAGGAGGGGCCAA 468
P E S P L Q S . P V I S F S S S T S L S P S | S E E S S S R E E G P S 89

[illegible][illegible]

11

P E I F G K A S E S L Q L V F G I D V K E A D P T G H S Y V L V T C 174
CCTGAGATCTTCGGCAAAGC CTCTGAGTCTTCGACGTGG TCTTTGGCAITGACGTGAAG GAAGCAGACCCACCGGCCA CTCCATATGTCCTTGTCACCT 723
CCTGTGATCTTCAGGAAAGC CCGTGAGTTCATAGAGATAC TTTTGGCAITTCCTGAGA GAAGTGGACCCCT...GATGA CTCCATATGTCCTTGTAACA 3191
P V I F R K A R E F I E I L F G I S L R E V D P . D D S Y V F V N T 979

L G L S Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G 207
GCCTAGGTCCTCCTATGAT GGCCTGCTGGTGATAATCA GATCATGCCCAAGACAGGCT TCCTGATAATTGCTCTGGTC ATGATTGCAATGGAGGGCGG 823
CATTAGACCTCACCTCTGAG GGGTGCTGAGTGATGAGCA GGGCATGTCCCAGAACCGCC TCCTGATTCTTATTCTGAGT ATCATCTTCATAAAGGGCAC 3291
L D L T S E G C L S D E O G M S Q N R L L I L I L S I I F I K G T 1012

—

II A P E E I W E E L S F M E V Y D G R E H S A Y G E P R K L L T	240
CCATGCTCTGAGGAGGANA TCTGGGAGGAGCTGAGTGTG ATGGAGGIGTATGATGGGAG GGAGCACAGTGCCTATGGGG AGCCAGGAAGCTGCTCACC	923
CTATGCCCTCTGAGGAGGTCA TCTGGGATGTGCTGAGTCCA AAGGGGTGCGTGGTGGGAG GGAGCACITTGCTTTGGGG AGCCAGGGAGCTCCTCACT	3391
Y A S E E V I W D V L S G I G Y R A G R E H F A F G E P R E L L T	1015

3

CCATGCTCCTGAGGAGGAMA TCTGGGAGGAGCTGAGTGTG ATGGAGGTCGTATGATGGGAG GGAGCACAGTGCCTATGGGG AGCCGAGGAGGAGCTGCTCACC 2410
CTATGCCCTCTGAGGAGGTCA TCTGGGATGTGCTGAGTGGCA AAGGGGTGCGTGGTGGGAG GGAGCACATTGCCCTTTGGGG AGCCGAGGAGGAGCTGCTCACC 923
Y A S E E V I W D V L S G I G V R A G R E H F A F G E P R E L L T 1015

FIG. 2(F)

Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P R A L A E T 274
 CAAGATTGGTGACGAGAAA GTACCTGGAGTACCGGCAGG TGCCGGACAGTGATCCCGCA CGCTATGAGTTCCTGTGGGG TCCAAGGGCCCTCGCTGAAA 1023
 AAAGTTGGGTGCAGGAACA TTACCTAGAGTACCGGGAGG TGCCCAACTCTCTCCCT CGTTACGAATTCCTGTGGGG TCCAAGAGCTCATTGAGAAG 3491
 < V W V Q E H Y L E Y R E V P N S S P P R Y E F L W G P R A H S E V 1079

S Y V K V L E Y V I K V S A R V R F F P S L R E A A L R E E E 307
 CCAGCTATGTGAAAGTCCTT GAGTATGTGATCAAGGTCAG TGCAAGAGTTCGCTTTTCT TCCATCCCTGCGTGAAGCA GCCTTGAGAGAGGAGGAAGA 1123
 TCATTAAGAGGAAAGTAGTA GAGTTTTGGCCATGCTAAA GAATACCGTCCCTATTACCT TTCCATCCTCTTACAAGGAT GCCTTGAAGATGTGGAAGA 3591
 I K R K V V E F L A M L K N T V P I T F P S S Y K D A L K D V E E 1112

G V OPA 309
 SGGAGTCTGAGCATGAGTTG CAGCCAAGGCCAGTGGAGG GGGACTGGGCCAGTGCACCT TCCAGGGCCGCTCCAGCAG CTTCCTCCCTGCTGTGAC 1223
 SAGAGCCCGGCCATATTG ACACCACAGATGATTCGACT GCCACAGAAAGTCAAGCTC CAGTGTCTATGCTCCCCAGCT TCTCTTCTGAGTGAAGTCTA 3691
 R A Q A I I D T T D S T A T E S A S S V M S P S F S S E OPA 1142

---ATGAGGCCCATCTTCA CTCGAAGAGAGCGGTCAGT GTTCTCAGTAGTAG----- GTTTC 1279
 GGGCAGATTCTCCCTCTGA GTTGAAGGGGGCAGTCGAG TTTCTACGTGGTGGAGGGCC TGGTTAGGCTGGAGAGAAC ACAGTGTATTGTCATTCT 3791

TGTTCTATTGGGTGACTGG AGATTATCTTTGTTCTTT TTGAATTGTCAAAATGTT TT--TTTAAAGGGATGGTTG AATGAACITTCAGCATCCAAG 1377
 GTTCCATATGGGTAGTATG GGGTTTACCTGTTTACTTT TGGGTATTTTCAAAATGCTT TTCTATTATAAACAGGTTT AATAGCTTCAGAATCCTAG 3891

TTTATGAATGACAGCAGT-C ACACAGTTCGTGTATATAG TTTAAGGGTAAGAGTCTTGT GTTTTATTCAGATTGGGAAA TCCATTCTATTTTGTGAATT 1476
 TTTATGCACATGAGTCGCAC ATGTATTGCTGTTTCTGG TTTAAGAGTAAACAGTTTGTAT ATTTTGTAACAAACAAAAACA CACCCAAACACACACCATG 3991

GGGATAATAACAGCAGTGG AATAGTACTTAGAATGTGA AAAATGAGCAGTAAATAGA TGAGATAAAGAACTAAAGAA ATTAAGAGATAGTCAATCT 1576
 GGAAACCTTCTGCCTCATT TTGTGATGTGTCACAGGITA ATGTGGTTTACGTAGGAA TTTTCTTGAACACTGTGAAGG AACCTGCGAGTTAAATAGTG 4091

TGCCTTATACCTCAGTCTAT TCTGTAAAATTTTAAAGAT ATAIGCATACCTGGATTCC TTGGCTTCTTTGAGAATGTA AGAGAAATTAATCTGAATA 1676
 GAATAAGTAAGGATTGT AATGTTTGCATTTCCTCAGG TCCCTTAGTCTGTGTTCTT GAAACTAAAGATACATACC TGGTTTGTCTGGCTTACGTA 4191

AAGAATTCTTCTCTG.....
 AGAAAGTAGAAGAAAGTAA CTGTAATAATAAA 1691
 4225

FIG. 3

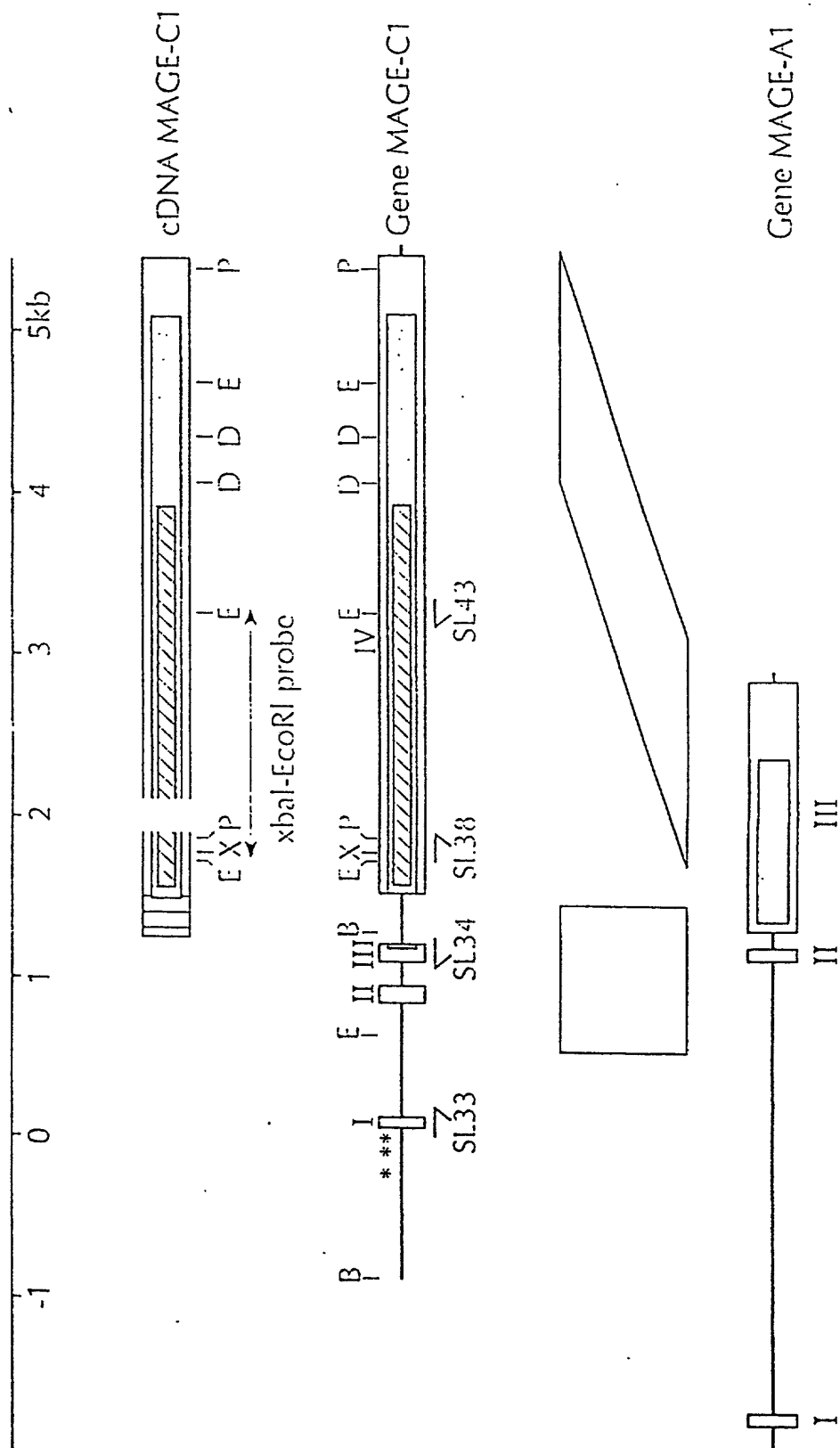


FIG. 4

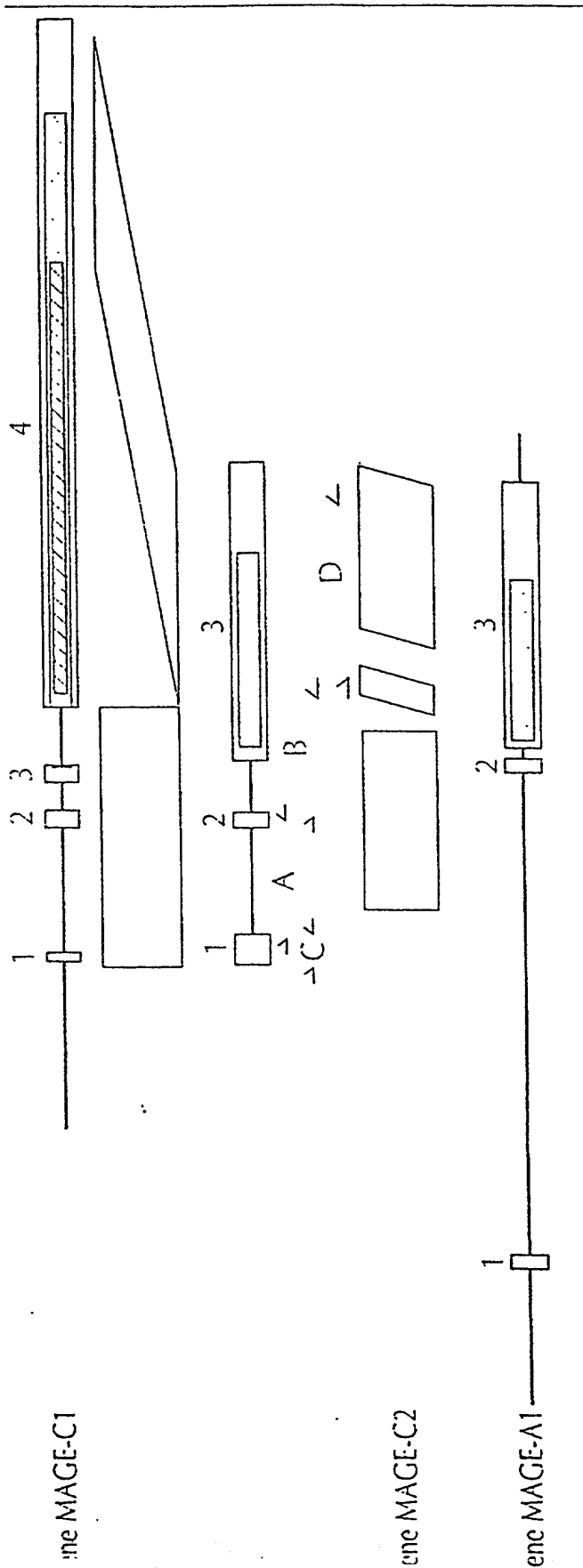


Figure 5 Nucleotide sequence of gene MAGE-C3
(SEQ ID NO: 21)

The sequence corresponds to nucleotides 3761 to 4801 of PAC clone 232G24 (GenBank accession number AL022152). It has been renumbered in this figure, taking as nucleotide number 1 the first nucleotide of the start codon.

Primers SL164 and SL165 that were used in the RT-PCR assay are indicated.

ATGCCTCTCTTTCCAAACCTTCCACGCCTCAGCTTTGAGGAAGACTTCCA	50
GAACCCGAGTGTGACAGAGGACTTGGTAGATGCACAGGATTCCATAGATG	100
AGGAGGAGGAGGATGCCTCCTCCACTTCCTCTTCTCTTTCCACTTTTTA	150
TTCCCCCTCTCCTCTTCTTGTCTCATCTCTCACCTTGTCTCACCCCTT	200
SL164	
ACCTCTACTCTCATTCTGGGTGTTCCAGAAGATGAGGATATGCCTGCTG	250
CTGGGATGCCACCTCTTCCCCAGAGTCTCTGAGATTCTCCCCAGGGT	300
CCTCCCAAGATCTCTCCCCAGGGTCTCCGCAGAGTCTCCCCAGAGTCC	350
TCTAGACTCCTGCTCATCCCCCTCTTTTGTGGACCCGATTGGATGAGGAGT	400
CCAGCAGTGAAGAGGAGGATACAGCTACTTGGCATGCCTTGCCAGAAAGT	450
GAATCCTTGCCAGGTATGCCCTGGATGAAAAGGTGGCTGAGTTGGTGCA	500
GTTTCTTCTCTCAAATATCAAACAAAAGAGCCTGTCACAAAGGCAGAGA	550
TGCTGACGACTGTCATCAAGAAGTATAAGGACTATTTTCCCATGATCTTC	600
GGGAAAGCCCATGAGTTCATAGAGCTAATTTTGGCATTGCCCTGACTGA	650
TATGGACCCCGACAACCACTCCTATTTCTTTGAAGACACATTAGACCTCA	700
CCTATGAGGGAAGCCTGATTGATGACCAGGGCATGCCCAAGAACTGTCTC	750
SL165	
CTGATTCTTATTCTCAGTATGATCTTCATAAAGGGCAGCTGTGTCCCCGA	800
GGAGGTCATCTGGGAAGTGTGAGTGCAATAGGGGTGTGTGCTGGGAGGG	850
AGCACTTTATATATGGGGATCCCAGAAAGCTGCTCACTATACATTGGGTG	900
CAGAGAAAGTACCTGGAGTACCGGGAGGTGCCCAACAGTGCTCCTCCACG	950
TTATGAATTTTTGTGGGGTCCAAGAGCCCATTCAGAGGCCAGCAAGAGAA	1000
GTCTTAGAGTTTTTATCCAAGCTATCCAGTATCATCCCTAG	1041

Figure 6 Amino-acid sequence of the putative MAGE-C3 protein (SEQ ID NO: 22)

5 MPLFPNLPRLSFEEDFQNPSVTEDLVDAQDSIDEEEDASSTSSSSFHFL 50
FPSSSSLSSSSPLSSPLPSTLILGVPEDEDMPAAGMPPLPQSPPEIPPQG 100
PPKISPQGPPQSPPQSPLDSCSSPLLWTRLDEESSSEEDTATWHALPES 150
ESLPRYALDEKVAELVQFLLLKYQTKEPVTKAEMLTTVIKKYKDYFPMIF 200
GKAHEFIELIFGIALTDMDPDNHSYFFEDTLDLTYEGSLIDDQGMPKNCL 250
LILILSMIFIKGSCVP EEVIWEVLSAIGVCAGREHFIYGDPRKLLTIHWV 300
10 QRKYLEYREVPNSAPPRYEFLWGPRAHSEASKRSLRVFIQAIQYHP 346

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201000.001500

Figure 7 Nucleotide sequence of gene MAGE-B5
(SEQ ID NO: 23)

This sequence is the antiparallel sequence corresponding to nucleotides 123358 to 124185 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL189 and SL190 that were used in the RT-PCR assay are indicated.

10	ATGACTTCTGCAGGTGTTTTTAATGCAGGATCTGACGAAAGGGCTAACAG	50
	TAGAGATGAGGAGTACCCATGTTCTCAGAGGTCTCACCTCCACTGAGA	100
	GTTTCATGCAGCAATTTTATAAATATTAAGGTGGGTTTGTGGAGCAGTTC	150
	CTGCTCTACAAGTTCAAAATGAAACAGCGTATTTTGAAGGAAGATATGCT	200
	GAAGATTGTCAACCCAAGATACCAAAACAGTTTGCTGAGATTACAGAA	250
15	GAGCTTCTGAGCACATTGAGGTGTCTTTGCAAGTTGACTTGAAGGAAGTC	300
	AACCCAACCTGTCACTTATATGACCTTGTCAGCAAGCTGAAACTCCCCAA	350
	CAATGGGAGGATTCATGTTGGCAAAGTGTTACCCAAGACTGGTCTCCTCA	400
	SL189	
	TGACTTTCCTGGTTGTGATCTTCCTGAAAGGCAACTGTGCCAACAAGGAA	450
20	GATACCTGGAAATTTCTGGATATGATGCAAATATATGATGGGAAGAAGTA	500
	CTACATCTATGGAGAGCCCAGGAAGCTCATCACTCAGGATTTTCGTGAGGC	550
	TAACGTACCTGGAGTACCACCAGGTGCCCTGCAGTTATCCTGCACACTAT	600
	CAATTCCTTTGGGGTCCAAGAGCCTATACTGAAACCAGCAAGATGAAAGT	650
25	CCTGGAATATTTGGCCAAGGTCAATGATATTGCTCCAGGTGCCTTCTCAT	700
	SL190	
	CACAATATGAAGAGGCTTTGCAAGATGAGGAAGAGAGCCCAAGCCAGAGA	750
	TGCAGCCGAAACTGGCACTACTGCAGTGGCCAAGACTGTCTCAGGGCGAA	800
	GTTTCAGCAGCTTCTCTCAACCCTATTGA	828

Figure 8 Amino-acid sequence of the putative MAGE-B5 protein (SEQ ID NO: 24)

	MTSAGVFNAGSDERANSRDEEYPCSSSEVSPSTESSCSNFINIKVGLLEQF	50
5	LLYKFKMKQRILKEDMLKIVNPRYQNQFAEIHRRASEHIEVVFAVDLKEV	100
	NPTCHLYDLVSKLKLPNNGRIHVGVLPKTGLLMTFLVVIFLKGNCANKE	150
	DTWKFLDMMQIYDGKKYIYGEPRKLITQDFVRLTYLEYHQVPCSYPAHY	200
	QFLWGPRAYTETSKMKVLEYLAKVNDIAPGAFSSQYEEALQDEEESPSQR	250
	CSRNWHYCSGQDCLRAKFSSFSQPY	275

10

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Figure 9 Nucleotide sequence of gene MAGE-B6
(SEQ ID NO: 25)

This sequence is the antiparallel sequence corresponding to nucleotides 146417 to 147640 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL191 and SL192 that were used in the RT-PCR assay are indicated.

10	ATGCCCTCGGGGTCACAAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGA	50
	GACCAATGGTCAGCCACAGGGTCTCAGGGTCCCCAGGCCACTGCAGAGA	100
	AGCAGGAAGAGTCCCACTCTTCTCATCTCTTCTCGCGCTGTCTGGGT	150
	SL191	
	GATTGTCTGTAGGTCTTCTGATGCCTCCATTCCTCAGGAGTCTCAGGGAGT	200
15	GTCACCCACTGGGTCTCCTGATGCAGTTGTTTCATATTCAAATCCGATG	250
	TGGCTGCCAACGGCCAAGATGAGAAAAGTCCAAGCACCTCCCGTGATGCC	300
	TCCGTTCCCTCAGGAGTCTCAGGGAGCTTACCCACTGGCTCTCCTGATGC	350
	AGGTGTTTTCAGGCTCAAATATGATGTGGCTGCCAACGGCCAAGATGAGA	400
	AAAGTCCAAGCACTTCCCATGATGTCTCCGTTCTCAGGAGTCTCAGGGA	450
20	GCTTACCCACTGGCTCGCCTGATGCAGGTGTTTCAGGCTCAAATATGA	500
	TGTGGCTGCCGAGGGTGAAGATGAGGAAAGTGTAAAGCGCTCACAGAAAG	550
	SL192	
	CCATCATTTTTTAAGCGCTTAAGCAAAGATGCTGTAAAGAAGAAGCGTGCT	600
	ACGTTGGCGCAATTCTTCGAGAAGAAGTTTGAGAAGAAGAGTCCATTTT	650
25	GAAGGCAGACATGCTGAAGTGTGTCCGAGAGAGTACAAGCCCTACTTCC	700
	CTCAGATCCTCAACAGAACCTCCCAACATTTGGTGGTGGCCTTTGGCGTT	750
	GAATTGAAAGAAATGGATTCCAGCGGCGAGTCTACACCCTTGTCAGCAA	800
	GCTAGGCCTCCCCAGTGAAGGAATTCTGAGTGGTGATAATGCGCTGCCGA	850
	AGTCGGGTCTCCTGATGTCTGCTCCTGGTTGTGATCTTCATGAACGGCAAC	900
30	TGTGCCACTGAAGAGGAGGTCTGGGAGTTCTGGGTCTGTTGGGGATATA	950
	TGATGGGATCCTGCATTCAATCTATGGGGATGCTCGGAAGATCATTACTG	1000
	AAGATTTGGTGCAAGATAAGTACGTGGTTTACGGGCAGGTGTGCAACAGT	1050
	GATCCTCCATGCTATGAGTTCCTGTGGGGTCCACGAGCCTATGCTGAAAC	1100
	CACCAAGATGAGAGTCTGCGTGTTTTGGCCGACAGCAGTAACACCAGTC	1150
35	CCGGTTTATACCCACATCTGTATGAAGACGCTTTGATAGATGAGGTAGAG	1200
	AGAGCATTGAGACTGAGAGCTTAA	1224

Figure 10 Amino-acid sequence of the putative MAGE-B6
protein (SEQ ID NO: 26)

	MPRGHKSKLRTCEKRQETNGQPQGLTGPDQATAEKQEESHSSSSSSSRACLG	50
5	DCRRSSDASIPQESQGVSPDGVSYSKSDVAANGQDEKSPSTSRDA	100
	SVPQESQGASPTGSPDAGVSGSKYDVAANGQDEKSPSTSHDVSVQESQG	150
	ASPTGSPDAGVSGSKYDVAAEGEDEESVSASQKAIIFKRLSKDAVKKKAC	200
	TLAQFLQKKFEKKESILKADMLKCVREYKPYFPQILNRTSQHLVVAFGV	250
	ELKEMDSSGESYTLVSKLGLPSEGILSGDNALPKSGLLMSLLVVFMMNGN	300
10	CATEEEVWEFLGLLGIYDGILHSIYGDARKIITEDLVQDKYVVYRQVCNS	350
	DPPCYEFLWGPAYAEETTKMRVLRVLADSSNTSPGLYPHLYEDALIDEVE	400
	RALRLRA	407

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